

## SEQUENCE LISTING

<110> Bayer AG

<120> ATP binding cassette genes and proteins for diagnosis  
and treatment of lipid disorders and inflammatory  
diseases

<130> ATP binding cassette genes and protein

<140>

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<150> 101706

<151> 1998-09-25

<160> 54

<170> PatentIn Ver. 2.0

<210> 1

<211> 6880

<212> DNA

<213> Human

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<223> cDNA of ABCA1 (ABC1)

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&lt;210&gt; 2

&lt;211&gt; 2201

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<213> Human

<223> Peptide sequence of ABCA1 (ABC1)

Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn  
1 5 10 15

Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly  
20 25 30

Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp  
35 40 45

Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp  
50 55 60

Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser  
65 70 75 80

Asn Leu Lys Leu Gln Asp Phe Leu Val Asp Asn Glu Thr Phe Ser Gly  
85 90 95

Phe Leu Tyr His Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met  
100 105 110

Leu Arg Ala Asp Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln  
115 120 125

Leu His Leu Thr Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile  
130 135 140

Gln Leu Gly Asp Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Arg Glu  
145 150 155 160

Table 1. Demographic characteristics of the study population	
Age (years)	50.0 ± 10.0
Gender	
Male	50.0%
Female	50.0%
Education (years)	12.0 ± 2.0
Marital status	
Married	80.0%
Single	20.0%
Occupation	
Professional	30.0%
Managerial	20.0%
Technical	10.0%
Service	20.0%
Unemployed	20.0%
Income (USD/month)	1000.0 ± 500.0
Health status	
Good	70.0%
Fair	30.0%

Lys Leu Ala Ala Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu  
165 170 175

Lys Pro Ile Leu Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys  
180 185 190

Glu Leu Ala Glu Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu  
195 200 205

Ala Gln Glu Leu Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu  
210 215 220

Val Met Phe Leu Thr Asn Val Asn Ser Ser Ser Ser Ser Thr Gln Ile  
225 230 235 240

Tyr Gln Ala Val Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Gly  
245 250 255

Leu Lys Ile Lys Ser Leu Asn Trp Tyr Glu Asp Asn Asn Tyr Lys Ala  
260 265 270

Leu Phe Gly Gly Asn Gly Thr Glu Glu Asp Ala Glu Thr Phe Tyr Asp  
275 280 285

Asn Ser Thr Thr Pro Tyr Cys Asn Asp Leu Met Lys Asn Leu Glu Ser  
290 295 300

Ser Pro Leu Ser Arg Ile Ile Trp Lys Ala Leu Lys Pro Leu Leu Val  
305 310 315 320

Gly Lys Ile Leu Tyr Thr Pro Asp Thr Pro Ala Thr Arg Gln Val Met  
325 330 335

Ala Glu Val Asn Lys Thr Phe Gln Glu Leu Ala Val Phe His Asp Leu  
340 345 350

Glu Gly Met Trp Glu Glu Leu Ser Pro Lys Ile Trp Thr Phe Met Glu

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355 360 365

Asn Ser Gln Glu Met Asp Leu Val Arg Met Leu Leu Asp Ser Arg Asp  
370 375 380

Asn Asp His Phe Trp Glu Gln Gln Leu Asp Gly Leu Asp Trp Thr Ala  
385 390 395 400

Gln Asp Ile Val Ala Phe Leu Ala Lys His Pro Glu Asp Val Gln Ser  
405 410 415

Ser Asn Gly Ser Val Tyr Thr Trp Arg Glu Ala Phe Asn Glu Thr Asn  
420 425 430

Gln Ala Ile Arg Thr Ile Ser Arg Phe Met Glu Cys Val Asn Leu Asn  
435 440 445

Lys Leu Glu Pro Ile Ala Thr Glu Val Trp Leu Ile Asn Lys Ser Met  
450 455 460

Glu Leu Leu Asp Glu Arg Lys Phe Trp Ala Gly Ile Val Phe Thr Gly  
465 470 475 480

Ile Thr Pro Gly Ser Ile Glu Leu Pro His His Val Lys Tyr Lys Ile  
485 490 495

Arg Met Asp Ile Asp Asn Val Glu Arg Thr Asn Lys Ile Lys Asp Gly  
500 505 510

Tyr Trp Asp Pro Gly Pro Arg Ala Asp Pro Phe Glu Asp Met Arg Tyr  
515 520 525

Val Trp Gly Gly Phe Ala Tyr Leu Gln Asp Val Val Glu Gln Ala Ile  
530 535 540

Ile Arg Val Leu Thr Gly Thr Glu Lys Lys Thr Gly Val Tyr Met Gln  
545 550 555 560

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Phe Glu Glu Gln Gly Ile Gly Val Gln Trp Asp Asn Leu Phe Glu Ser  
740 745 750

[illegible]



Pro Val Glu Glu Asp Gly Phe Asn Leu Thr Thr Ser Val Ser Met Met  
755 760 765

Leu Phe Asp Thr Phe Leu Tyr Gly Val Met Thr Trp Tyr Ile Glu Ala  
770 775 780

Val Phe Pro Gly Gln Tyr Gly Ile Pro Arg Pro Trp Tyr Phe Pro Cys  
785 790 795 800

Thr Lys Ser Tyr Trp Phe Gly Glu Glu Ser Asp Glu Lys Ser His Pro  
805 810 815

Gly Ser Asn Gln Lys Arg Ile Ser Glu Ile Cys Met Glu Glu Glu Pro  
820 825 830

Thr His Leu Lys Leu Gly Val Ser Ile Gln Asn Leu Val Lys Val Tyr  
835 840 845

Arg Asp Gly Met Lys Val Ala Val Asp Gly Leu Ala Leu Asn Phe Tyr  
850 855 860

Glu Gly Gln Ile Thr Ser Phe Leu Gly His Asn Gly Ala Gly Lys Thr  
865 870 875 880

Thr Thr Met Ser Ile Leu Thr Gly Leu Phe Pro Pro Thr Ser Gly Thr  
885 890 895

Ala Tyr Ile Leu Gly Lys Asp Ile Arg Ser Glu Met Ser Thr Ile Arg  
900 905 910

Gln Asn Leu Gly Val Cys Pro Gln His Asn Val Leu Phe Asp Met Leu  
915 920 925

Thr Val Glu Glu His Ile Trp Phe Tyr Ala Arg Leu Lys Gly Leu Ser  
930 935 940

Glu Lys His Val Lys Ala Glu Met Glu Gln Met Ala Leu Asp Val Gly

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102250-52998760

Ala Lys Glu Gly Ala Phe Val Glu Leu Phe His Glu Ile Asp Asp Arg  
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1170 1175 1180

Glu Glu Ile Phe Leu Lys Val Ala Glu Glu Ser Gly Val Asp Ala Glu  
1185 1190 1195 1200

Thr Ser Asp Gly Thr Leu Pro Ala Arg Arg Asn Arg Arg Ala Phe Gly  
1205 1210 1215

Asp Lys Gln Ser Cys Leu Arg Pro Phe Thr Glu Asp Asp Ala Ala Asp  
1220 1225 1230

Pro Asn Asp Ser Asp Ile Asp Pro Glu Ser Arg Glu Thr Asp Leu Leu  
1235 1240 1245

Ser Gly Met Asp Gly Lys Gly Ser Tyr Gln Val Lys Gly Trp Lys Leu  
1250 1255 1260

Thr Gln Gln Gln Phe Val Ala Leu Leu Trp Lys Arg Leu Leu Ile Ala  
1265 1270 1275 1280

Arg Arg Ser Arg Lys Gly Phe Phe Ala Gln Ile Val Leu Pro Ala Val  
1285 1290 1295

Phe Val Cys Ile Ala Leu Val Phe Ser Leu Ile Val Pro Pro Phe Gly  
1300 1305 1310

Lys Tyr Pro Ser Leu Glu Leu Gln Pro Trp Met Tyr Asn Glu Gln Tyr  
1315 1320 1325

Thr Phe Val Ser Asn Asp Ala Pro Glu Asp Thr Gly Thr Leu Glu Leu  
1330 1335 1340

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Lys Gly Trp His Ala Ile Ser Ser Phe Leu Asn Val Ile Asn Asn Ala

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                         965                      970                      975  
Met Gln Arg Lys Leu Ser Val Ala Leu Ala Phe Val Gly Gly Ser Lys  
                         980                      985                      990  
Val Val Ile Leu Asp Glu Pro Thr Ala Gly Val Asp Pro Tyr Ser Arg  
                         995                      1000                      1005  
Arg Gly Ile Trp Glu Leu Leu Lys Tyr Arg Gln Gly Arg Thr Ile  
                         1010                      1015                      1020  
Ile Leu Ser Thr His His Met Asp Glu Ala Asp Val Leu Gly Asp Arg  
1025                      1030                      1035                      1040  
Ile Ala Ile Ile Ser His Gly Lys Leu Cys Cys Val Gly Ser Ser Leu  
                         1045                      1050                      1055  
Phe Leu Lys Asn Gln Leu Gly Thr Gly Tyr Tyr Leu Thr Leu Val Lys  
                         1060                      1065                      1070  
Lys Asp Val Glu Ser Ser Leu Ser Ser Cys Arg Asn Ser Ser Ser Thr  
                         1075                      1080                      1085  
Val Ser Tyr Leu Lys Lys Glu Asp Ser Val Ser Gln Ser Ser Ser Asp  
                         1090                      1095                      1100  
Ala Gly Leu Gly Ser Asp His Glu Ser Asp Thr Leu Thr Ile Asp Val  
1105                      1110                      1115                      1120  
Ser Ala Ile Ser Asn Leu Ile Arg Lys His Val Ser Glu Ala Arg Leu  
                         1125                      1130                      1135  
Val Glu Asp Ile Gly His Glu Leu Thr Tyr Val Leu Pro Tyr Glu Ala  
                         1140                      1145                      1150

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Ile Leu Arg Ala Asn Leu Gln Lys Gly Glu Asn Pro Ser His Tyr Gly  
1555 1560 1565

Ile Thr Ala Phe Asn His Pro Leu Asn Leu Thr Lys Gln Gln Leu Ser  
1570 1575 1580

Glu Val Ala Pro Met Thr Thr Ser Val Asp Val Leu Val Ser Ile Cys  
1585 1590 1595 1600

Val Ile Phe Ala Met Ser Phe Val Pro Ala Ser Phe Val Val Phe Leu  
1605 1610 1615

Ile Gln Glu Arg Val Ser Lys Ala Lys His Leu Gln Phe Ile Ser Gly  
1620 1625 1630

Val Lys Pro Val Ile Tyr Trp Leu Ser Asn Phe Val Trp Asp Met Cys  
1635 1640 1645

Asn Tyr Val Val Pro Ala Thr Leu Val Ile Ile Ile Phe Ile Cys Phe  
1650 1655 1660

Gln Gln Lys Ser Tyr Val Ser Ser Thr Asn Leu Pro Val Leu Ala Leu  
1665 1670 1675 1680

Leu Leu Leu Leu Tyr Gly Trp Ser Ile Thr Pro Leu Met Tyr Pro Ala  
1685 1690 1695

Ser Phe Val Phe Lys Ile Pro Ser Thr Ala Tyr Val Val Leu Thr Ser  
1700 1705 1710

Val Asn Leu Phe Ile Gly Ile Asn Gly Ser Val Ala Thr Phe Val Leu  
1715 1720 1725

Glu Leu Phe Thr Asp Asn Lys Leu Asn Asn Ile Asn Asp Ile Leu Lys  
1730 1735 1740

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Ser Val Phe Leu Ile Phe Pro His Phe Cys Leu Gly Arg Gly Leu Ile  
1745 1750 1755 1760

Asp Met Val Lys Asn Gln Ala Met Ala Asp Ala Leu Glu Arg Phe Gly  
1765 1770 1775

Glu Asn Arg Phe Val Ser Pro Leu Ser Trp Asp Leu Val Gly Arg Asn  
1780 1785 1790

Leu Phe Ala Met Ala Val Glu Gly Val Val Phe Phe Leu Ile Thr Val  
1795 1800 1805

Leu Ile Gln Tyr Arg Phe Phe Ile Arg Pro Arg Pro Val Asn Ala Lys  
1810 1815 1820

Leu Ser Pro Leu Asn Asp Glu Asp Glu Asp Val Arg Arg Glu Arg Gln  
1825 1830 1835 1840

Arg Ile Leu Asp Gly Gly Gly Gln Asn Asp Ile Leu Glu Ile Lys Glu  
1845 1850 1855

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1860 1865 1870

Cys Val Gly Ile Pro Pro Gly Glu Cys Phe Gly Leu Leu Gly Val Asn  
1875 1880 1885

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1890 1895 1900

Val Thr Arg Gly Asp Ala Phe Leu Asn Arg Asn Ser Ile Leu Ser Asn  
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Ile His Glu Val His Gln Asn Met Gly Tyr Cys Pro Gln Phe Asp Ala  
1925 1930 1935

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1940 1945 1950

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1955 1960 1965

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1970 1975 1980

Tyr Ser Gly Gly Asn Lys Arg Lys Leu Ser Thr Ala Met Ala Leu Ile  
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Leu Asp Arg Glu Asp Leu His Cys Asp Ile Asp Glu Thr Cys His Phe  
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<400> 22

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<210> 23

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<213> Human

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<213> Human

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<220>

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<212> DNA

<213> Human

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<213> Human

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